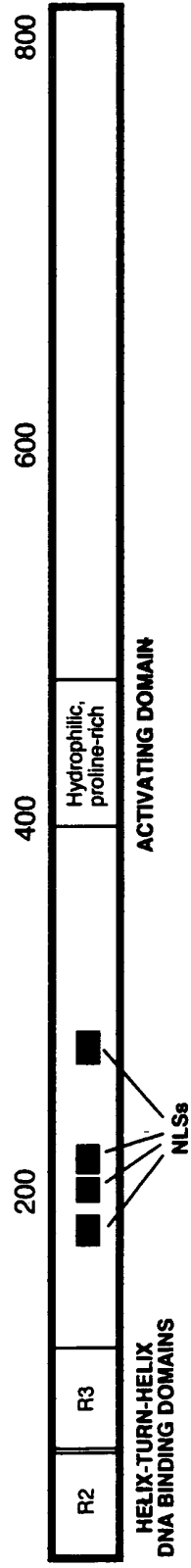


MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARW 50  
 YEWLDPSIKKTEWSREEEEKLLHLAKLMPTQWRTIAPIIGRTAAQCLEHY 100  
 EFLLDKAAQRDNEEETTDDPRKLKPGEIDPNPETKPARPDPIDMDEDELE 150  
 MLSEARARLANTQGGKAKRKAREKQLEEARRLAALQKRRELRAAGIEIQK 200  
 KRKRKRGV DYN AEIPFEKKPALGFYDTSEENYQALDADFRKLRQQDL DGE 250  
 LRSEKEGRDRKKDKOHLKRKESDLPSAILQTSGVSEFTKKRSKLVLPAP 300  
 QISDAELQEVVKVGQASEIARQTAEESGITNSASSTLLSEYNVTNNSVAL 350  
 RTPRTPASQDRILQEAQNLMA L TNVD TPLKGG LNTPLHESDFSGVTPORO 400  
 VVQTPNTVLSTPFRTPSNGAEG L TPRS GTTPKPVINSTPGRTPLRDKLNI 450  
 NPEDGMADYSDPSYVKOMERESREHLRLGLLGLPAPKNDFEIVLPENAEK 500  
 ELEEREIDDTYIEDAADVDARKQAIRDAERVKEMKRMHKAVQKDLPRPSE 550  
 VNETILRPLNVEPPLTDLQKSEELIKKEMITMLHYDLLHHPYEPSGNKKG 600  
 KTVGFGTNNSEHITYLEHNPYEKFSKEELKKAQDVLVQEME VVKQGM SHG 650  
 ELSSEAYNQVWEECY SQVLYLPGQSR YTRANLASKKDRIESLEKRLEINR 700  
 GHMTTEAKRAAKMEKKMKILLGGYQSRAMGLMKQLNDLWDQIEQAHLER 750  
 TFEELKKHEDSAIPRRLECLKEDVQRQQEREKELQHRYADLLLEKETLKS 800

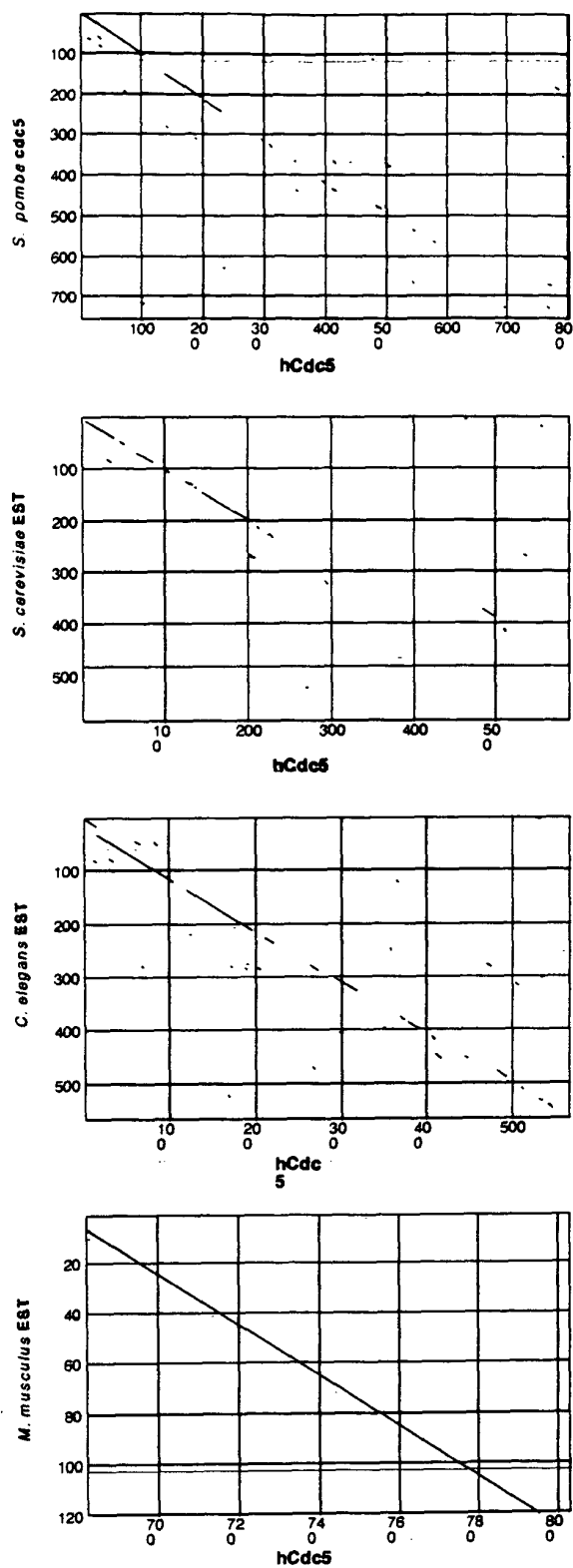
KF\*

Fig. 1A



**Fig. 1B**

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**Fig. 2A**



hCdc5	PLKGGGLNTPLHESDFSGVTPQRQVVQTPNTVLSTPFRTSPNSGAEGLTPRSGLTPKPVINSTP (378-439)
<i>S. pombe</i> cdc5	SVTIEVRNQLMNREQSSLLGQESIPLQPGGTGYTGVTPSHAANGS---ALAAP--Q--ATP (380-434)
b-Myb	PVK-TL--PFSPSQFLNFWNKQDTLEESPSLTSTPVCSQKVVTTPHLDKTPHQAFAAF (445-503)
a-Myb	ILRKKRMRVGHSPGSEL-RDGSUNDGGNMALKTPLKTPFSPSQFFNTCPGNEQLNIENPSF (446-508)
hCdc5	GRTPLRDKLNINPEDGMADYSDPSYVKQMERESREHLRLGLLPAPKNDFEIVLPENAEK (440-500)
<i>S. pombe</i> cdc5	FRTPR-DTFSINAAERAGR-LASE-REN-KIRLKALRELLAKLPKPNKYEL-ME-P-R- (435-487)
b-Myb	VTPDQKYSMDNTRHTP-TPFKNAKYGPKLPQTPHLEEDLKEVLRSEAGIELIIEDDIRP (504-565)
a-Myb	TSTPICGQKAL-ITTPHKEITPKDQKENVGFRTPTIRRSILGTPTPTPFKNALAAQEKK (509-569)

**Fig. 2C**

5' untranslated region:

GGCAGGAGAGGAAGTGGCGGCTTTGAGTCCGGTGGCCCAATCGCTGTTACTACTTCTCTGAAGCTCCTCTCGGCTGCTTGC  
CGAGACACCTTGGCCCAAG

Coding region:

1 DNA BINDING DOMAIN (\_\_\_)

1 atgcctcgaa ttatgatcaa gggggggcga tggaggaata ccgaggatga aattctgaaa  
61 gcagcggtaa tgaatatatg gaaaaatcag tggcttagga ttgcctcatt cctgcataga  
121 aaatcagcaa agcagtgcaa agccagatgg targaatggc tggatccaaq catlaagaaq  
181 acagaatggt ccagagaaga agaggaaaaa ctcttgacact tggccaaggt gatgccaact  
241 cagtggagga ccattgctcc aatcattgga agaacagcgg cccagtgctt agaacactat  
301 gaatttcttc tggataaagc tgcccaaaga gacaatgaag aggaacaac agatgatcca  
361 cgaaaactta aacctggaga aatagatcca aatccagaaa caaaaccagc gcggcctgat  
421 ccaattgata tggatgagga tgaacttgag atgctttctg aagccagagc ccgcttggtc

2 NUCLEAR LOCALIZATION DOMAIN (....)

481 aatactcagg gaaagaaggc caagaggaaa gcaagagaga aacaattgga agaagcaaga  
541 cgtcttgctg ccttccaaaa aagaagagaa ctgcgagcag ctggcataga aattcagaag  
601 aaaaagaaaa ggaagagagg agttgattat aatgccgaaa tccattttga aaaaagcct  
661 gcccttggtt tttatgatac ttctgaggaa aactaccaag ctcttgacgc agatttcagg  
721 aaattaagac aacaggatct tcatggggag ctaagatctg aaaaagaagg aagagataga  
781 aaaaaagaca aacagcattt gaaaaggaaa aaagaatctg attaccatc agctattctt  
841 caaactagtg gtgtttctga atttactaaa aagagaagca aactagtact tctgccccct  
901 cagatttcag atgcagaact ccaggaagtt gtaaaagtag gccaaagcag tgaatttga  
961 cgtcaaaact cagaggaatc tggcataaca aattctgctt ccagtacact tttgtctgag  
1021 tacaatgtca ccaacaacag cgttgctctt agaacaccac gaacaccagc ttcccaggac  
1081 agaattctgc aggaagccca gaacctcatg gccctcacca atgtggacac cccattgaaa

3 ACTIVATING DOMAIN (\_\_\_)

1141 ggtggactta ataccctcatt gcatgagagt gacttctcag gtgtaactcc acagcgacaa  
1201 gttgtacaga ctccaaacac agttctctct actccattca ggactccttc taatggagct  
1261 gaagggctga ctccccggag tggaaacaact cccaaaccag ttattaactc tactccgggt  
1321 agaactcctc ttcgagacaa gttaaacatt aatccccgag atggaatggc agactatagt  
1381 gatccctctt acgtgaagca gatggaaaaga gaatccccgag aacatctccg tttagggttg  
1441 ttgggccttc ctgcccctaa gaatgatttt gaaattgttc taccagaaaa tgcgagaag  
1501 gagctggaag aacgtgaaat agatgatact tacattgaag atgctgctga tgtggatgct  
1561 cgaaagcagg ccatacgaga tgcagagcgt gtaaggaaa tgaacgaat gcataaagct  
1621 gtccagaaag atctgccaag accatcagaa gtaaatgaaa ctattctaag acccttaa  
1681 gtagaaccgc cttaacaga tttacagaaa agtgaagaac taatcaaaaa agaaatgatc  
1741 acaatgcttc attatgacct tctacatcac ccttatgaac catctggaaa taaaaaaggc  
1801 aaaactgtag ggtttggtag caataattca gagcacatta cctatctgga acataatcct  
1861 tatgaaaagt tctccaaaga agagctgaaa aaggcccagg atgttttggg gcaggagatg  
1921 gaagtgggta aacaaggaat gagccatgga gagctctcaa gtgaagctta taaccagggtg  
1981 tgggaagaat gctacagtca agttttatat ctctctgggc agagccgcta cacacgggccc  
2041 aatctggcta gtaaaaagga cagaattgaa tcacttgaaa agaggctcga gataaacagg  
2101 ggtcacatga cgacagaagc caagagggct gcaaatgatg aaaagaagat gaaaattttg  
2161 cttggggggt accagtctcg tgctatgggg ctcatgaaac agttgaatga cttatgggac  
2221 caaattgaac aggtcactt ggagttacgc acttttgaag aactcaagaa acatgaagat  
2281 tctgctattc cccggaggct agagtgtcta aaagaagacg ttcagcgaca acaagaaaga  
2341 gaaaaggaac ttcaacatag atatgctgat ttgctgctgg agaaagagac tttaaagtca  
2401 aaattctga

3' untranslated region:

AGTACAGTTTATATCTGTACAGGATTAAATTAATGCGGTTTTCATACTCTAGAAGGCTGAAACTG ATGTTTATCTTCATTGACA  
AATTTACCCACCATCTGTGGTTTTTTCAGTTGTTTTTAAATGATATCGATCTTACACATCTGTGTATAAAGACCTTAACCCACA  
GGACGGACATTTTAGAGTTTAAATTATTA AGGCTATCATCTTTTAGTAATGTCATATTTGCAAAGTTTTTGTGTTTTGCGCTTTAA  
TTTAAAAAGCCTAATTTTAAAGTGCTGCGCTGTGAGTAACTCTTGAATAAAAAACAAATATAAAAA

Fig. 2D

FIG. 3

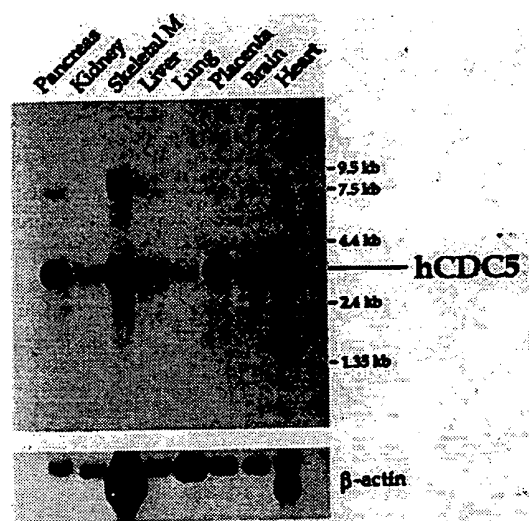
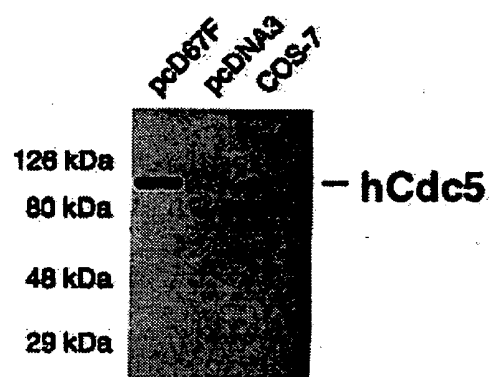


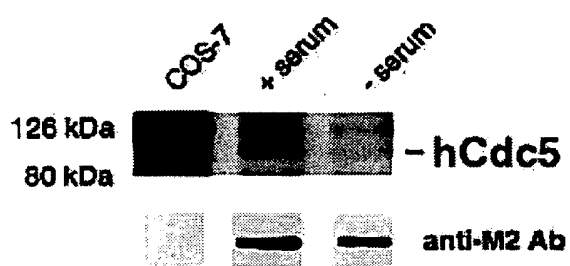
FIG. 3



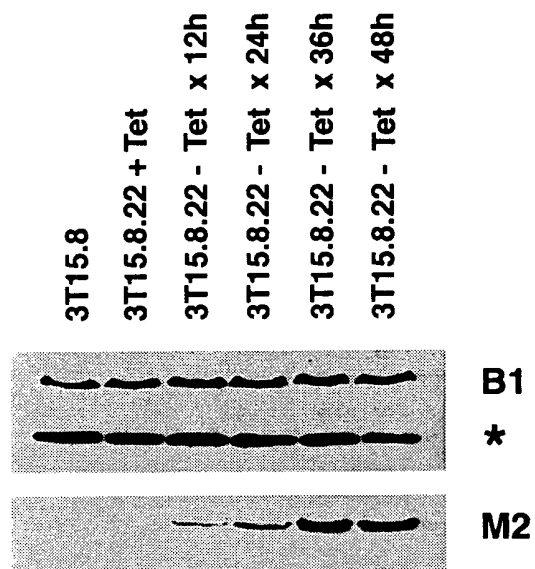
**FIG. 4A**



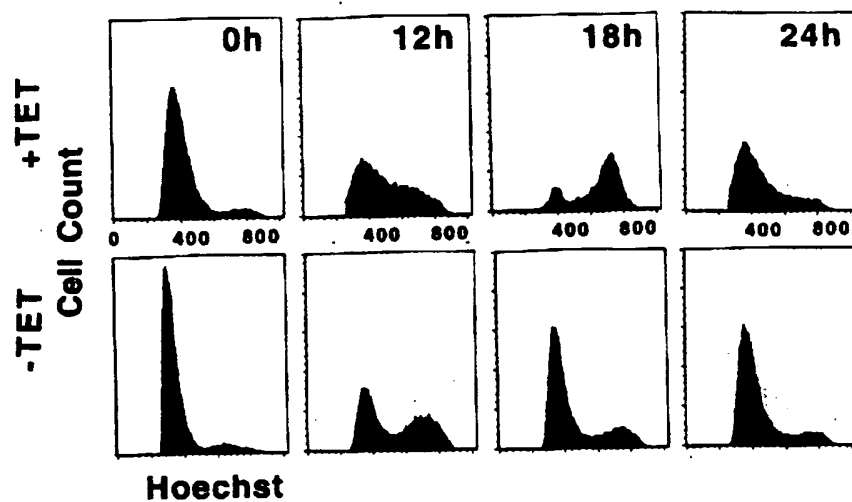
09757049 040804



**FIG. 4B**



**FIG. 5**



**Fig. 6**

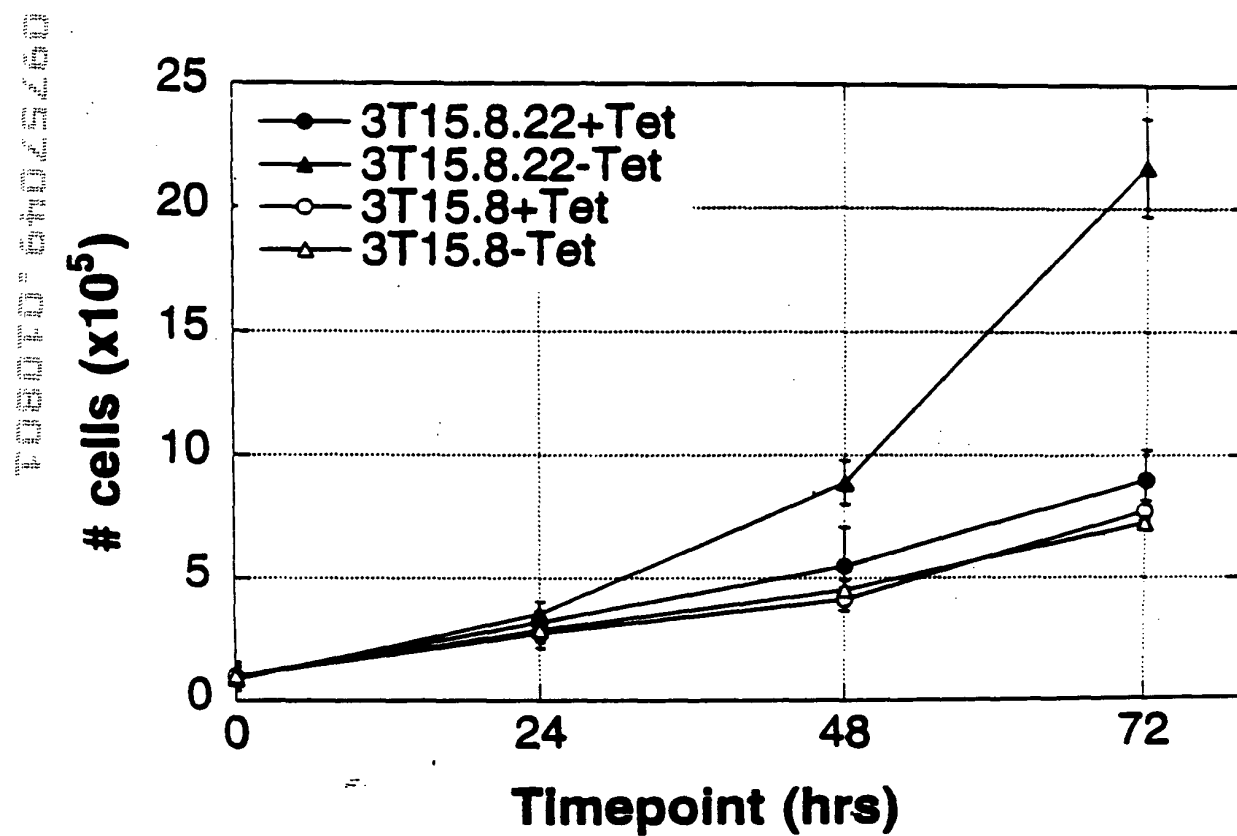
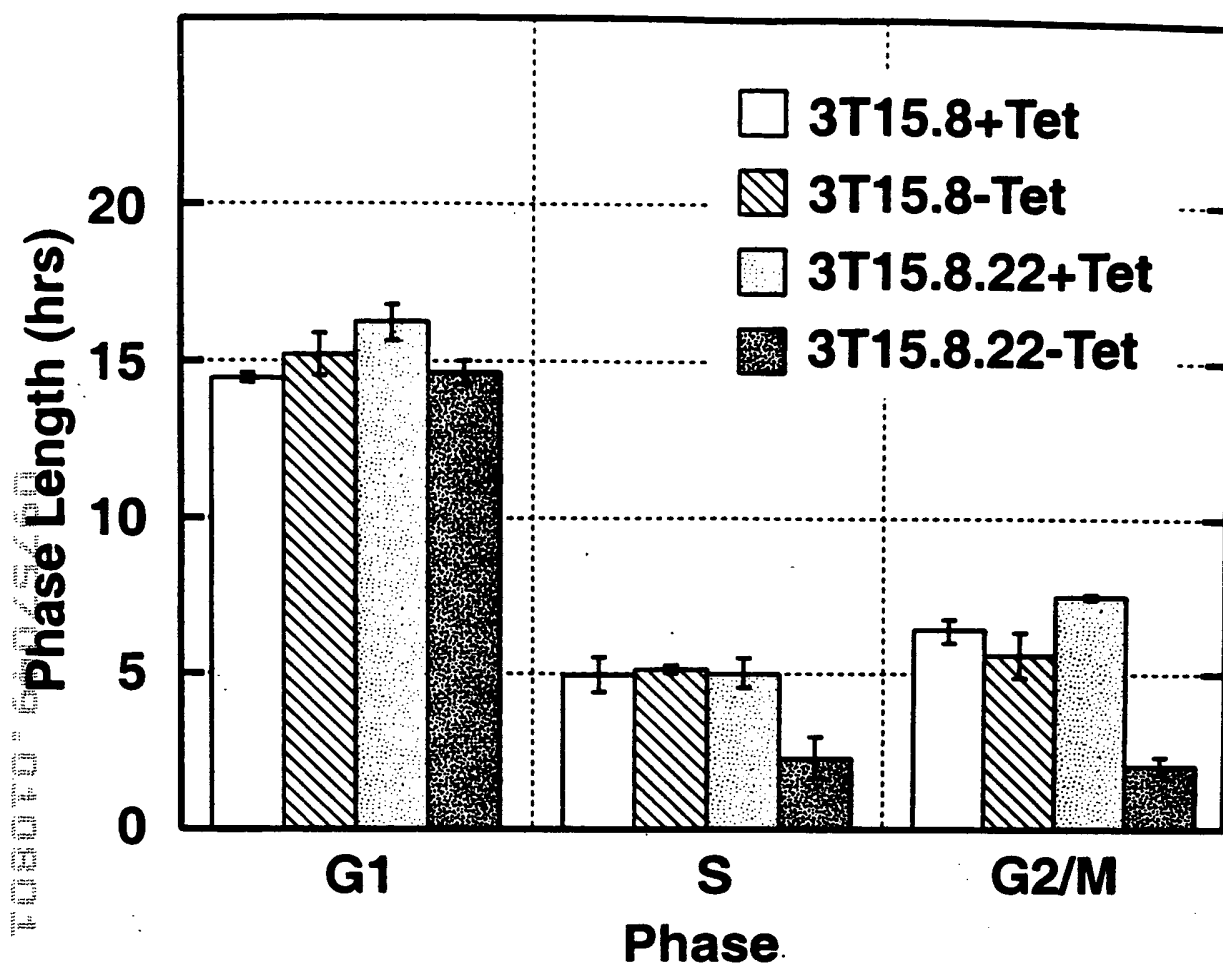


Fig. 7



**FIG. 8**

00000 04025260

Cell size by FSc  
(arbitrary units)

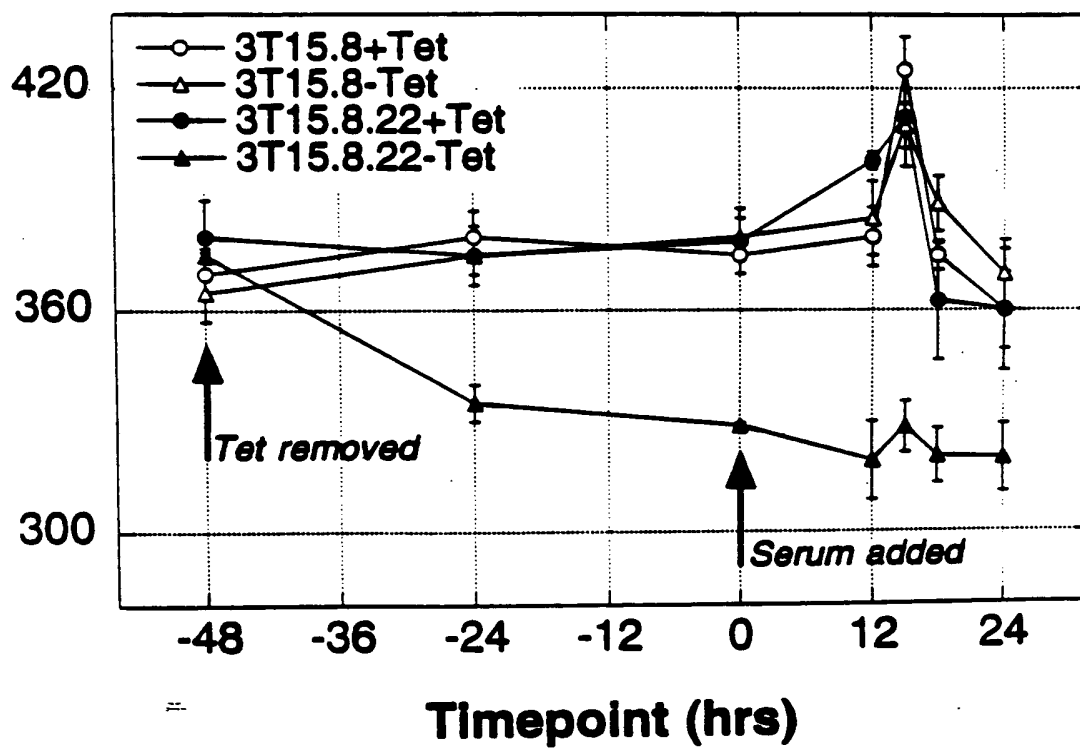


Fig. 9

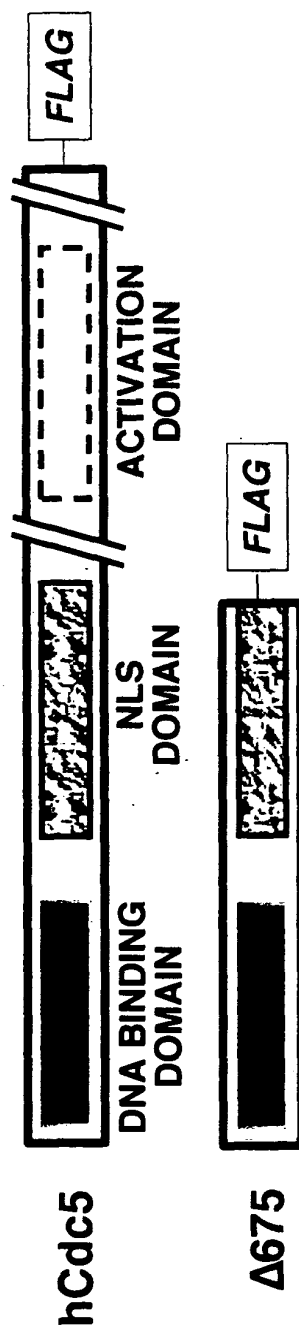


Fig. 10

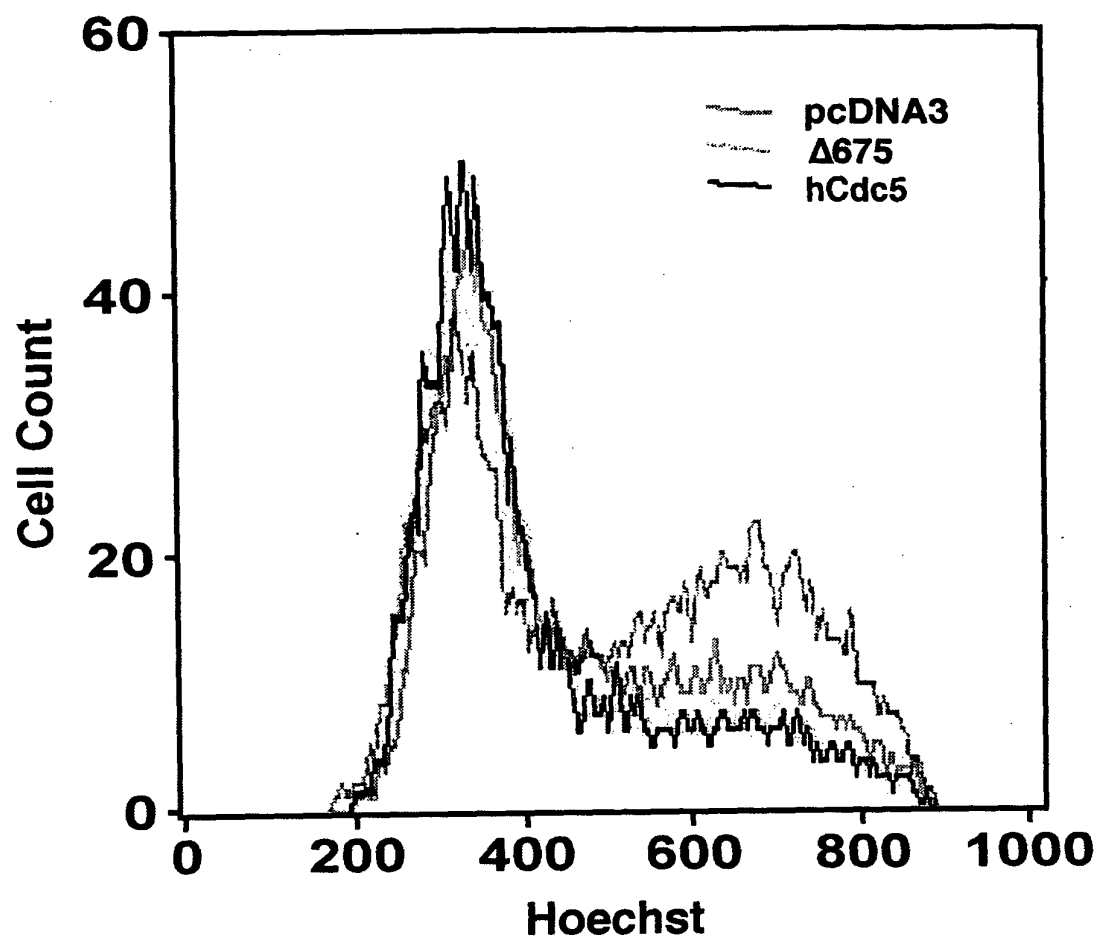


FIG. 11



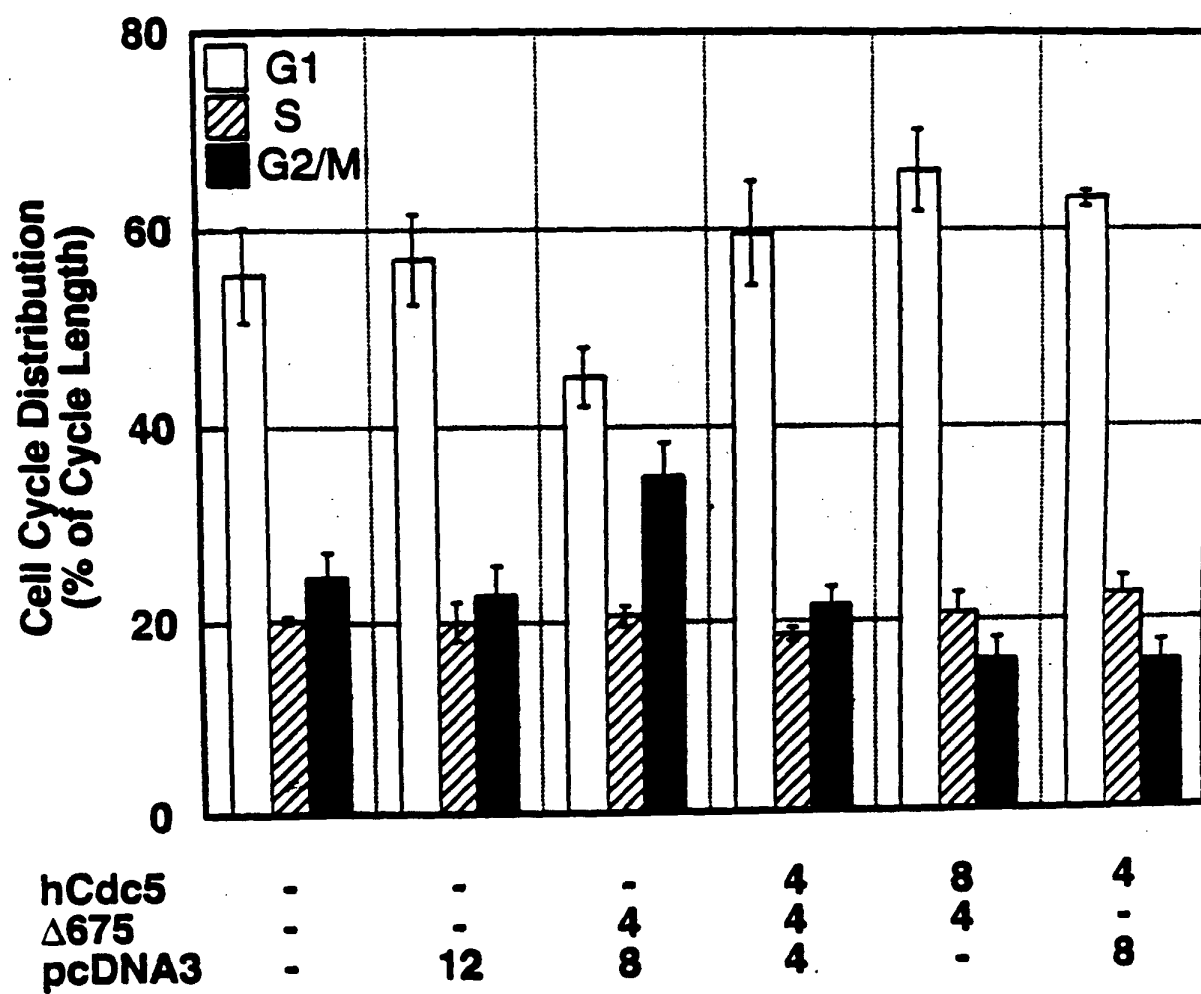


Fig. 12

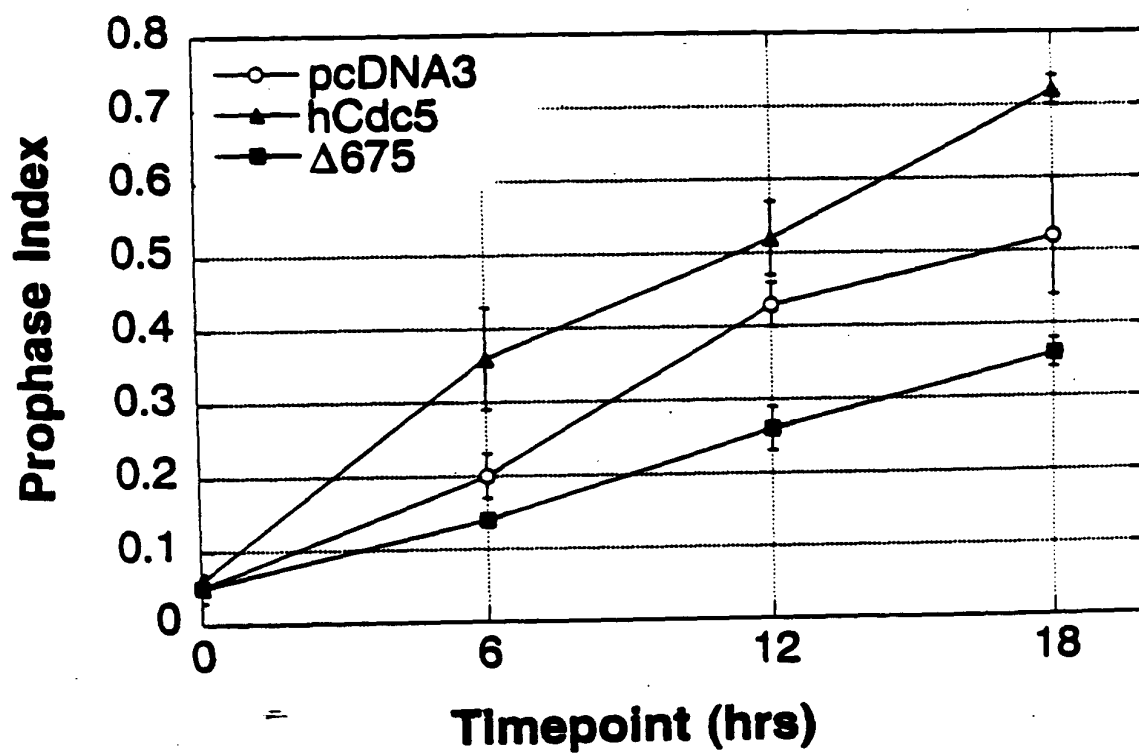
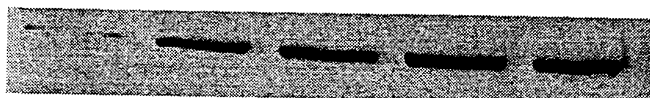
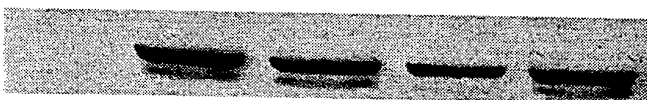


Fig. 13

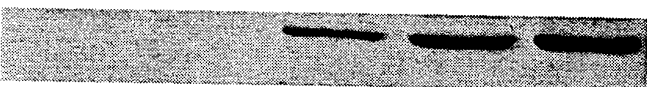
0 12 15 18 21 hrs



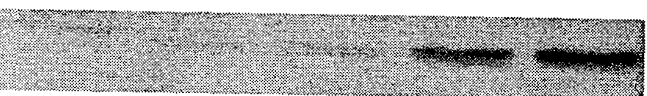
**hCdc5**



**p50 CLNE**

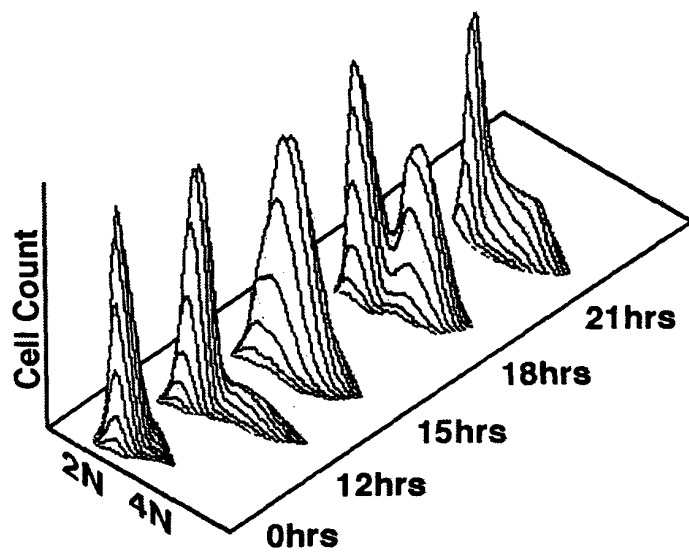


**p60 CLNA**



**p62 CLNB1**

**FIG. 14A**



**FIG. 14B**

Consensus G A T T T A A C A T A A (SEQ ID NO:13)

8.05 G A T T T A A C A T A A  
8.04 G A T T T A A C A T A A  
8.03 G A T T T A A C A T A A  
8.02 G A T T T A A C A T A A  
8.01 G A T T T A A C A T A A

6.05 G G T G T A A C G T G G (SEQ ID NO:36)  
6.04 G T G T T A C C A C A T (SEQ ID NO:37)  
6.03 C C A T A A A T T T A G (SEQ ID NO:38)  
6.02 G A G A T A A A G T C T (SEQ ID NO:39)  
6.01 G T G T T A T T G A A A (SEQ ID NO:40)

3.05 A C C C A C G T C T A T (SEQ ID NO:41)  
3.04 G G T T A G G A T A G G (SEQ ID NO:42)  
3.03 G T T G A G T A G T A T (SEQ ID NO:43)  
3.02 C T G T T A A T T T C C (SEQ ID NO:44)  
3.01 G G T G T T A T T G A T (SEQ ID NO:45)

FIG 15